RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/078,927B
Source: IFW16
Date Processed by STIC: 06-22-2005

ENTERED

IFW16

RAW SEQUENCE LISTING DATE: 06/22/2005
PATENT APPLICATION: **US/10/078,927B** TIME: 17:07:57

Input Set : **A:\SJ-01-0032 Revised 0305.ST25.txt**
Output Set: **N:\CRF4\06222005\J078927B.raw**

```
      3 <110> APPLICANT: St. Jude Children's Research Hospital
      4       St. Jude Children's Research Hospital
      5       Curran, Thomas
      6       Keshvara, Lakhu
      8 <120> TITLE OF INVENTION: Cyclin Dependent Kinase 5 Phosphorylation of Disabled 1
Protein
     10 <130> FILE REFERENCE: SJ-01-0032
     12 <140> CURRENT APPLICATION NUMBER: 10/078,927B
     13 <141> CURRENT FILING DATE: 2002-02-19
     15 <160> NUMBER OF SEQ ID NOS: 4
     17 <170> SOFTWARE: PatentIn version 3.2
     19 <210> SEQ ID NO: 1
     20 <211> LENGTH: 6
     21 <212> TYPE: PRT
     22 <213> ORGANISM: Mus musculus
     25 <220> FEATURE:
     26 <221> NAME/KEY: DOMAIN
     27 <222> LOCATION: (1)..(6)
     28 <223> OTHER INFORMATION: smallest carboxy terminal Dab1 tryptic fragment containing a
Cdk5
     29       phosphorylation site
     31 <220> FEATURE:
     32 <221> NAME/KEY: SITE
     33 <222> LOCATION: (3)..(3)
     34 <223> OTHER INFORMATION: Serine at residue #3 equates to Serine491 in mouse Dab1
sequence
     35       Cdk5 phosphorylation of Serine requires a Proline (P) in the +1
     36       position and a Lysine (K) in the +3 position
     38 <400> SEQUENCE: 1
     40 Gln Ser Ser Pro Ser Lys
     41 1               5
     44 <210> SEQ ID NO: 2
     45 <211> LENGTH: 24
     46 <212> TYPE: PRT
     47 <213> ORGANISM: Mus musculus
     50 <220> FEATURE:
     51 <221> NAME/KEY: DOMAIN
     52 <222> LOCATION: (1)..(24)
     53 <223> OTHER INFORMATION: Dab1 tryptic fragment containing a Cdk5 phosphorylation site
     55 <220> FEATURE:
     56 <221> NAME/KEY: SITE
     57 <222> LOCATION: (21)..(21)
     58 <223> OTHER INFORMATION: Serine at Reisdue 21 equates to Serine515 in mouse Dab1
sequence
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59 Cdk5 phosphorylation of Serine requires a Proline (P) in the +1
60 position and a Lysine (K) in the +3 position
62 <400> SEQUENCE: 2

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```
64 Ser Ser Ala Ser His Val Ser Asp Pro Thr Ala Asp Asp Ile Phe Glu
65 1               5                   10                  15
68 Glu Gly Phe Glu Ser Pro Ser Lys
69             20
72 <210> SEQ ID NO: 3
73 <211> LENGTH: 14
74 <212> TYPE: PRT
75 <213> ORGANISM: Mus musculus
78 <220> FEATURE:
79 <221> NAME/KEY: DOMAIN
80 <222> LOCATION: (1)..(14)
81 <223> OTHER INFORMATION: Dab1 phosphopeptide domain used for antibody production
83 <220> FEATURE:
84 <221> NAME/KEY: MOD_RES
85 <222> LOCATION: (8)..(8)
86 <223> OTHER INFORMATION: PHOSPHORYLATION, equates to Serine491 in mouse Dab1 sequence
87       Cdk5 phosphorylation of Serine requires a Proline (P) in the +1
88       position and a Lysine (K) in the +3 position
90 <400> SEQUENCE: 3
92 Thr Pro Ala Pro Arg Gln Ser Ser Pro Ser Lys Ser Ser Ala
93 1               5                   10
96 <210> SEQ ID NO: 4
97 <211> LENGTH: 555
98 <212> TYPE: PRT
99 <213> ORGANISM: Mus musculus
101 <400> SEQUENCE: 4
103 Met Ser Thr Glu Thr Glu Leu Gln Val Ala Val Lys Thr Ser Ala Lys
104 1               5                   10                  15
107 Lys Asp Ser Arg Lys Lys Gly Gln Asp Arg Ser Glu Ala Thr Leu Ile
108             20                  25                  30
111 Lys Arg Phe Lys Gly Glu Gly Val Arg Tyr Lys Ala Lys Leu Ile Gly
112         35                  40                  45
115 Ile Asp Glu Val Ser Ala Ala Arg Gly Asp Lys Leu Cys Gln Asp Ser
116     50                  55                  60
119 Met Met Lys Leu Lys Gly Val Val Ala Gly Ala Arg Ser Lys Gly Glu
120 65                  70                  75                  80
123 His Lys Gln Lys Ile Phe Leu Thr Ile Ser Phe Gly Gly Ile Lys Ile
124                 85                  90                  95
127 Phe Asp Glu Lys Thr Gly Ala Leu Gln His His His Ala Val His Glu
128             100                 105                 110
131 Ile Ser Tyr Ile Ala Lys Asp Ile Thr Asp His Arg Ala Phe Gly Tyr
132         115                 120                 125
135 Val Cys Gly Lys Glu Gly Asn His Arg Phe Val Ala Ile Lys Thr Ala
136     130                 135                 140
139 Gln Ala Ala Glu Pro Val Ile Leu Asp Leu Arg Asp Leu Phe Gln Leu
140 145                 150                 155                 160
143 Ile Tyr Glu Leu Lys Gln Arg Glu Glu Leu Glu Lys Lys Ala Gln Lys
144                 165                 170                 175
147 Asp Lys Gln Cys Glu Gln Ala Val Tyr Gln Thr Ile Leu Glu Glu Asp
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```
148                 180                 185                 190
151 Val Glu Asp Pro Val Tyr Gln Tyr Ile Val Phe Glu Ala Gly His Glu
152         195                 200                 205
155 Pro Ile Arg Asp Pro Glu Thr Glu Glu Asn Ile Tyr Gln Val Pro Thr
156     210                 215                 220
159 Ser Gln Lys Lys Glu Gly Val Tyr Asp Val Pro Lys Ser Gln Pro Val
160 225                 230                 235                 240
163 Ser Ala Val Thr Gln Leu Glu Leu Phe Gly Asp Met Ser Thr Pro Pro
164                 245                 250                 255
167 Asp Ile Thr Ser Pro Pro Thr Pro Ala Thr Pro Gly Asp Ala Phe Leu
168                 260                 265                 270
171 Pro Ser Ser Ser Gln Thr Leu Pro Gly Ser Ala Asp Val Phe Gly Ser
172         275                 280                 285
175 Met Ser Phe Gly Thr Ala Ala Val Pro Ser Gly Tyr Val Ala Met Gly
176     290                 295                 300
179 Ala Val Leu Pro Ser Phe Trp Gly Gln Gln Pro Leu Val Gln Gln Gln
180 305                 310                 315                 320
183 Ile Ala Met Gly Ala Gln Pro Pro Val Ala Gln Val Ile Pro Gly Ala
184                 325                 330                 335
187 Gln Pro Ile Ala Trp Gly Gln Pro Gly Leu Phe Pro Ala Thr Gln Gln
188                 340                 345                 350
191 Ala Trp Pro Thr Val Ala Gly Gln Phe Pro Pro Ala Ala Phe Met Pro
192         355                 360                 365
195 Thr Gln Thr Val Met Pro Leu Ala Ala Ala Met Phe Gln Gly Pro Leu
196     370                 375                 380
199 Thr Pro Leu Ala Thr Val Pro Gly Thr Asn Asp Ser Ala Arg Ser Ser
200 385                 390                 395                 400
203 Pro Gln Ser Asp Lys Pro Arg Gln Lys Met Gly Lys Glu Ser Phe Lys
204                 405                 410                 415
207 Asp Phe Gln Met Val Gln Pro Pro Pro Val Pro Ser Arg Lys Pro Asp
208                 420                 425                 430
211 Gln Pro Ser Leu Thr Cys Thr Ser Glu Ala Phe Ser Ser Tyr Phe Asn
212         435                 440                 445
215 Lys Val Gly Val Ala Gln Asp Thr Asp Asp Cys Asp Asp Phe Asp Ile
216     450                 455                 460
219 Ser Gln Leu Asn Leu Thr Pro Val Thr Ser Thr Thr Pro Ser Thr Asn
220 465                 470                 475                 480
223 Ser Pro Pro Thr Pro Ala Pro Arg Gln Ser Ser Pro Ser Lys Ser Ser
224                 485                 490                 495
227 Ala Ser His Val Ser Asp Pro Thr Ala Asp Asp Ile Phe Glu Glu Gly
228                 500                 505                 510
231 Phe Glu Ser Pro Ser Lys Ser Glu Glu Gln Glu Ala Pro Asp Gly Ser
232         515                 520                 525
235 Gln Ala Ser Ser Thr Ser Asp Pro Phe Gly Glu Pro Ser Gly Glu Pro
236     530                 535                 540
239 Ser Gly Asp Asn Ile Ser Pro Gln Asp Gly Ser
240 545                 550                 555
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VERIFICATION SUMMARY DATE: 06/22/2005
PATENT APPLICATION: **US/10/078,927B** TIME: 17:07:58

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